## IN THE CLAIMS

Please replace claims 1 and 49 with the following amended claims. A marked up version of the claims, indicating the changes made, is attached hereto as appendix A.

1. (Three times amended) A method for designing a specific polyamide

$$X_1X_2...X_{m-\gamma-X_{(m+1)}}...X_{(2m-1)}X_{2m}-R_1$$

wherein

 $X_1$ ,  $X_2$ ,  $X_m$ ,  $X_{(m+1)}$ ,  $X_{(2m-1)}$ , and  $X_{2m}$  are carboxamide residues forming carboxamide binding pairs  $X_1/X_{2m}$ ,  $X_2/X_{(2m-1)}$ ,  $X_m/X_{(m+1)}$ ,

 $\gamma$  is  $\gamma$ -aminobutyric acid or 2,4 diaminobutyric acid, and

 $R_1$  is  $-NH(CH_2)_{0-100}NR_2R_3$ ,  $-NH(CH_2)_{0-12}CONH(CH_2)_{0-100}NR_2R_3$ , or  $-NHR_2$ , where  $R_2$  and  $R_3$  are independently selected from the group consisting of H, Cl, NO, N-acetyl, benzyl,  $C_{1-100}$  alkyl,  $C_{1-100}$  alkylamine,  $C_{1-100}$  alkyldiamine,  $C_{1-$ 

- (a) identifying a target sequence of double stranded DNA having the form 5'- $WN_1N_2$  ...  $N_mW$ -3',  $N_1N_2$ ...  $N_m$  being the sequence to be bound by carboxamide residues, wherein each N is independently chosen from the group A, G, C, and T, each W is independently chosen from the group A and T, and M is an integer having a value from M to M:
- (b) representing the identified sequence as 5'-Wab ... xW-3', wherein a is a first nucleotide to be bound by the  $X_1$  carboxamide residue, b is a second nucleotide to be bound by the  $X_2$  carboxamide residue, and x is the corresponding nucleotide to be bound by the  $X_m$  carboxamide residue;
- (c) defining a as A, G, C, or T to correspond to the first nucleotide to be bound by a carboxamide residue in the identified sequence;
- (d) selecting Im as the  $X_1$  carboxamide residue and Py as the  $X_{2m}$  carboxamide residue if a = G;
- (e) selecting Py as the  $X_1$  carboxamide residue and Im as the  $X_{2m}$  carboxamide residue if a = C;
- (f) selecting Hp as the  $X_1$  carboxamide residue and Py as the  $X_{2m}$  carboxamide residue if a = T;
- (g) selecting Py as the  $X_1$  carboxamide residue and Hp as the  $X_{2m}$  carboxamide residue if a = A; and
- (h) repeating steps c g for b through x until all carboxamide residues are selected; wherein Im is N-methylimidazole, Hp is 3-hydroxy-N-methylpyrrole, Py is N-methylpyrrole, A is adenine, G is guanine, C is cytosine, and T is thymine.

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49. (Twice Amended) A polyamide designed by the method of claim 1, having the structure:

wherein

R<sub>4</sub> is selected from the group consisting of H, NH<sub>2</sub>, SH, Cl, Br, F, N-acetyl, and N-formyl;

R<sub>5</sub> is H or NH<sub>2</sub>;

 $R_1$  is  $-NH(CH_2)_{0-100}NR_2R_3$ ,  $-NH(CH_2)_{0-12}CONH(CH_2)_{0-100}NR_2R_3$ , or  $-NHR_2$ , where  $R_2$  and  $R_3$  are independently selected from the group consisting of H, Cl, NO, N-acetyl, benzyl,  $C_{1-100}$  alkyl,  $C_{1-100}$  alkylamine,  $C_{1-100}$  alkyldiamine,  $C_{1-100}$  alkylcarboxylate,  $C_{1-100}$  alkenyl, a  $C_{1-100}$  alkynyl, and  $C_{1-100}$  alkyl-L, where L is selected from the group consisting of arylboronic acids, biotins, polyhistidines comprised from about 2 to 8 amino acids, haptens, solid phase supports, oligodeoxynucleotides, N-ethylnitrosourea, fluorescein, bromoacetamide, iodoacetamide, DL- $\alpha$ -lipoic acid, acridine, captothesin, pyrene, mitomycin, texas red, anthracene, anthrinilic acid, avidin, DAPI, and oligodeoxynucleotide, isosulfan blue, malachite green, psoralen, ethyl red, 4-(psoraen-8-yloxy)-butyrate, tartaric acid, and (+)- $\alpha$ -tocopheral;

each X is independently selected from the group consisting of N, CH, and COH; each a is an integer from 2 to 5; and each b is an integer from 3 to 6.

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